UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/966,781	09/28/2001	Patricia Soulard	A0000281-66-MG	3811

7590 06/17/2004

Mehdi Ganjeizadeh
Warner-Lambert Company
2800 Plymouth Road
Ann Arbor, MI 48105

EXAMINER	
RAMIREZ, DELIA M	

ART UNIT	PAPER NUMBER
1652	

DATE MAILED: 06/17/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/966,781	SOULARD, PATRICIA	
	Examiner	Art Unit	
	Delia M. Ramirez	1652	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *07 May 2004*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-67* is/are pending in the application.

4a) Of the above claim(s) *12-18,20-52 and 54-67* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-11,19 and 53* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on _____ is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☒ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *1/16/2002*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: Alignment

DETAILED ACTION

Status of the Application

Claims 1-67 are pending.

Applicant's election with traverse of Group I, claims 1-11, 19, 53, drawn in part to a polypeptide having phosphodiesterase activity wherein said polypeptide comprises the amino acid sequence of SEQ ID NO: 1, in a communication filed on 5/7/2004 is acknowledged.

Applicant's traverse is on the ground(s) that the restriction creates 37 groups which on average result in 2 claims per invention. Furthermore, applicants argue that the restriction requirement is even more restrictive since a single claim may be included in several groups. Applicants request the consolidation of all groups within one classification. Applicants also submit that such consolidation will not impose an undue burden on the Office. According to Applicants, no allegation of burden has been made for inventions within the same classification.

Applicant's arguments have been fully considered but are not deemed persuasive to withdraw the restriction requirement. While it is agreed that some claims have been included in several groups, this was required by the fact that in some cases these claims were generic and could be applied to different groups or due to the fact that some of these claims encompass several inventions within each claim. In regard to the fact that some of the groups were assigned the same classification, it is noted that sharing the same classification only implies that the inventions belong to the general classification but does not indicate that they are the same invention. It was clearly indicated in the previous Office Action as to the reasons why each of the groups, including those sharing the same classification, encompassed distinct or independent inventions. In regard to the burden of search, it is noted that a comprehensive search of all groups would require not only a class/subclass search for all the groups, but it will also require a sequence as well as patented/non-patented literature search for each of the groups indicated. The class/subclass

search would not preclude a sequence and/or patented/non-patented literature search. Therefore, an undue burden would be imposed on the Office if all the groups were to be examined.

The requirement is deemed proper and therefore is made FINAL.

Claims 12-18, 20-52, 54-67 are withdrawn from further consideration by the Examiner, 37 CFR 1.142(b), as being drawn to a non-elected invention.

Specification

1. The specification is objected for not complying with sequence rules. Specifically, Figure 1 discloses a sequence, no sequence identifier is shown in Figure 1, and the Brief Description of the Drawings does not refer to a specific sequence identifier in regard to Figure 1. See particularly 37 CFR 1.821(d). Appropriate correction is required.

2. The specification is objected to due to the recitation of "aminoacid". This term is recited throughout the disclosure. It is suggested that the term be replaced with "amino acid". Appropriate correction is required.

Priority

3. Acknowledgment is made of a claim for foreign priority under 35 U.S.C. 119(a)-(d) to EP 0042026837 filed on 09/28/2000.

Information Disclosure Statement

4. The information disclosure statement (IDS) submitted on 1/16/2002 is acknowledged. The submission is in compliance with the provisions of 37 CFR 1.97. Accordingly, the information disclosure statement is being considered by the examiner.

Claim Objections

5. Claims 2-11, 19, and 53 are still partially drawn to non-elected inventions. Examination of such claims will be restricted to the subject matter elected, which in the instant case is the polypeptide of SEQ ID NO: 1. Applicants are requested to amend the claims accordingly in response to this Office Action.

6. Claims 1, 19 and 53 are objected to because of the recitation of "PDE7" and "L22M2". Abbreviations unless otherwise obvious and/or commonly used in the art, should not be recited in the claims without at least once reciting the entire phrase for which the abbreviation is used. It is suggested that the term "phosphodiesterase 7" be recited at least once next to the term "PDE7" in parentheses. Appropriate correction is required.

7. Claim 3 is objected to due to the recitation of the term "aminoacid". It should be replaced with "amino acid". Appropriate correction is required.

8. Claims 19 and 53 are objected to as not being in proper form as required by 37 CFR 1.75. They are multiple dependent claims which depend from other multiple dependent claims , i.e. claims 10, 11. Appropriate correction is required.

9. Claims 19 and 53 are objected to as they refer to non-elected claims, i.e. claims 12-18. For examination purposes, references to non-elected claims will be given no patentable weight. Appropriate correction is required.

10. Claim 53 is objected to due to the recitation of the term "measures". For clarity, it is suggested that the term be replaced with "measurements". Appropriate correction is required.

Claim Rejections - 35 USC § 101

11. 35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

12. Claims 1-11, 19 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter.

13. Claims 1-11 and 19, as written, do not sufficiently distinguish over polypeptides as they exist naturally because the claims do not particularly point out any non-naturally occurring differences between the claimed products and the naturally occurring products. In the absence of the hand of man, the naturally occurring products are considered non-statutory subject matter. See *Diamond v. Chakrabarty*, 447 US 303, 206 USPQ 193 (1980). The claims should be amended to indicate the hand of the inventor, e.g., by insertion of "isolated" or "purified" as taught by Examples 1 and 2 of the specification. See MPEP 2105.

Claim Rejections - 35 USC § 112, Second Paragraph

14. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

15. Claims 1-11, 19 and 53 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

16. Claim 1 (claims 2-11, 19 and 53 dependent thereon) is indefinite in the recitation of "a polypeptide possessing a ...activity at least about 6 fold, preferably about 8 or 10 fold, most preferably 15 to 20 fold higher than.....with the exception of the amino acid sequence disclosed by Michaeli et al.....(L22M2)" for the following reasons. First, the term "at least about" is contradictory because the term "about" can be interpreted as "less than" whereas the term "at least" is synonym of "no less than". In addition, it is unclear if the term "preferably about 8 or 10 fold, most preferably 15 to 20 fold higher than.." is further limiting the phosphodiesterase activity. The term "higher than the phosphodiesterase catalytic activity of an endogenous full length PDE7 protein...." is unclear as one cannot determine which

specific polypeptide is being as the basis of comparison. An endogenous full length PDE7 protein which comprises at least the catalytic domain of the PDE7, as recited, encompasses many proteins. As such, the basis of comparison, i.e. the endogenous full length PDE7 protein, is variable. Thus, while the claimed polypeptide may have at least 6 fold higher activity with respect to one of the PDE7 proteins recited, the same polypeptide may have a different activity with respect to another PDE7 protein. Furthermore, the recitation of "with the exception of the amino acid sequence disclosed by Michaeli et al.....(L22M2)" is an improper incorporation by reference. The polypeptide being excluded from the scope of the claim should be referred to by its own sequence identifier. For examination purposes, the claim will be interpreted as being directed to a polypeptide having phosphodiesterase catalytic activity. Correction is required.

17. Claims 3-6 (claims 10-11, 19, and 53 dependent thereon) is indefinite in the recitation of "427" since the polypeptide of SEQ ID NO: 1 only contains 426 amino acids. For examination purposes, it will be assumed that the term "427" reads "426". Correction is required.

18. Claims 10-11 (claims 19 and 53 dependent thereon) are indefinite in the recitation of "at least X% homology or identity, preferably X% homology or identity, ..." for the following reasons. As known in the art, while how to calculate sequence identity is well defined, how sequence homology is calculated depends upon how the term "homology" is defined. In most cases, the calculation of homology takes into consideration mismatches and whether substitutions are conservative. While the term "identity" has been disclosed in the specification, no definition of the term "homology" has been presented. As such, it is unclear if Applicants are equating identity with homology by using the term "homology or identity" or if homology is intended to be different from identity. In addition, the term "preferably X% homology or identity" is unclear and confusing since one cannot determine if the term is further limiting the degree of homology or identity. For examination purposes, it will be assumed that the claims recite "a polypeptide

having at least 80% sequence identity with a polypeptide as defined in any one of claims 1-9". Correction is required.

19. Claim 19 is indefinite in the recitation of "wherein PDE7(A) is of human, mouse or rat origin, most preferably human" for the following reasons. There is no antecedent basis for the term "PDE7(A)" and it is unclear as to what a phosphodiesterase 7A is. Furthermore, the term "most preferably human" is unclear and confusing since one cannot determine if the term is further limiting the origin of the polypeptide. For examination purposes, it will be assumed that the claim reads "wherein the polypeptide is of human, mouse or rat origin". Correction is required.

Claim Rejections - 35 USC § 112, First Paragraph

20. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

21. Claims 1-9, 19 and 53 rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claims 1, 19 and 53 are directed to a genus of polypeptides having phosphodiesterase catalytic activity. Claims 2-9 are directed in part to the genus of polypeptides described above with the added limitation that they comprise a PDE7 catalytic domain and wherein said polypeptides are structural homologs of a polypeptide comprising at least 312 amino acids of the polypeptide of SEQ ID NO: 1. See claim interpretation in Claim Rejections under 35 USC 112, second paragraph. While the specification discloses a human, rat and mouse PDE7, the specification is silent in regard to (1) the structure of other phophodiesterases (2) other structural homologs of a polypeptide comprising at least 312 amino acids of

the polypeptide of SEQ ID NO: 1 with the exception of the polypeptides of SEQ ID NO: 2 and 3, (3) the structural elements in any phosphodiesterase which would provide the desired degree of enzymatic activity, or (4) the structural elements in any 312 consecutive amino acids of the polypeptide of SEQ ID NO: 1 which can be modified to create a structural homolog with PDE7 activity.

The genus of polypeptides claimed is a large, structurally variable genus. While a sufficient written description of a genus of polypeptides may be achieved by a recitation of a representative number of polypeptides defined by their amino acid sequence or a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus., in the instant case, either (1) there is no structural feature which is representative of all the members of the genus of phosphodiesterases recited in the claim or (2) the structural recitation recited, i.e. homolog of a polypeptide comprising at least 312 consecutive amino acids of the polypeptide of SEQ ID NO: 1, does not constitute a substantial portion of the genus as the remainder of any polypeptide comprising said structural elements is completely undefined and the specification does not define the remaining structural features for members of the genus to be selected. It is noted that no degree of structural homology has been recited. Furthermore, while one could argue that the recited genus of polypeptides is adequately described by the polypeptide of SEQ ID NO: 1, since one could use structural homology using the structure of SEQ ID NO: 1 and those known in the art to isolate other phosphodiesterases as claimed, it is noted that the art teaches the unpredictability of using structural homology to accurately determine function and even a high degree of structural homology may not result in functional homology. Witkowski et al. (Biochemistry 38:11643-11650, 1999) teaches that one amino acid substitution transforms a β-ketoacyl synthase into a malonyl decarboxylase and completely eliminates β-ketoacyl synthase activity. Seffernick et al. (J. Bacteriol. 183(8):2405-2410, 2001) teaches that two naturally occurring Pseudomonas enzymes having 98% amino acid sequence identity catalyze two different reactions: deamination and dehalogenation, therefore having different function. Broun et al. (Science

282:1315-1317, 1998) teaches that as few as four amino acid substitutions can convert an oleate 12-desaturase into a hydrolase and as few as six amino acid substitutions can transform a hydrolase to a desaturase. Therefore, in the absence of any additional information correlating structure with phosphodiesterase activity, or any correlation between SEQ ID NO: 1 and phosphodiesterase activity, many structurally unrelated polypeptides are encompassed by the genus. The specification only discloses a few species of the genus, i.e. SEQ ID NO: 1-3, which is insufficient to put one of ordinary skill in the art in possession of all attributes and features of all species within the genus of polypeptides claimed. Therefore, one skilled in the art cannot reasonably conclude that the applicant had possession of the claimed invention at the time the instant application was filed.

22. Claims 1-11, 19 and 53 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for the polypeptide of SEQ ID NO: 1, does not reasonably provide enablement for (1) any phosphodiesterase, or (2) any polypeptide comprising a PDE7 catalytic domain which is a structural homolog of a polypeptide comprising at least 312 amino acids of the polypeptide of SEQ ID NO: 1. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

The criteria for undue experimentation, summarized in *re Wands*, 8, USPQ2nd 1400 (Fed. Cir. 1988) are: 1) quantity of experimentation necessary, 2) the amount of direction or guidance presented, 3) the presence and absence of working examples, 4) the nature of the invention, 5) the state of prior art, 6) the relative skill of those in the art, 7) the predictability or unpredictability of the art, and 8) the breath of the claims.

The scope of the claims is not commensurate with the enablement provided in regard to the large number of unknown phosphodiesterases encompassed by the claims. As indicated above, while the

polypeptide of SEQ ID NO: 1 has been disclosed, there is no disclosure of the structure of other phophodiesterases, other structural homologs of a polypeptide comprising at least 312 amino acids of the polypeptide of SEQ ID NO: 1 with the exception of the polypeptides of SEQ ID NO: 2 and 3, the structural elements which should be present in any phosphodiesterase such that the desired level of enzymatic activity is obtained, or the structural elements in any 312 consecutive amino acids of the polypeptide of SEQ ID NO: 1 which can be modified to create a structural homolog with PDE7 activity.

The art as discussed above, teaches the unpredictability of isolating proteins of similar function based solely on structural homology and indicates that even high structural homology does not always results in functional homology. Since structure determines function, one of skill in the art would require some knowledge or guidance as to which are the structural elements which are characteristic of any phosphodiesterase, any polypeptide having PDE7 activity, or which are the structural elements which would allow a phosphodiesterase to display the desired level of phosphodiesterase activity. Therefore, due to the lack of relevant examples, the amount of information provided, the lack of knowledge about the critical structural elements required to display the desired function, and the unpredictability of the prior art in regard to function based on homology, one of ordinary skill in the art would have to go through the burden of undue experimentation in order to screen and isolate those polypeptides having any phosphodiesterase activity or PDE7 activity recited in the claims. Thus, Applicant has not provided sufficient guidance to enable one of ordinary skill in the art to make and use the invention in a manner reasonably correlated with the scope of the claims.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless -

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

23. Claims 1-11, 19 and 53 are rejected under 35 U.S.C. 102(b) as being anticipated by Han et al. (J. Biol. Chem. 272(26):16152-16157, 1997). Han et al. teaches a human alternative splicing variant of the cAMP-specific phosphodiesterase PDE7 labeled HCP1 (HSPDE7A1). The splice variant of Han et al. is identical to HCP1 except that the first 26 amino acids are missing (Figure 1A). The splice variant of Han et al. is 456 amino acids long. The PDE7 of Han et al. comprises all of SEQ ID NO: 1. See attached alignment provided for visualization purposes. Claims 1-11 and 19 are directed in part to a human, mouse or rat phosphodiesterase comprising a phosphodiesterase 7 catalytic domain and at least 312 amino acids of SEQ ID NO: 1. It is noted that while claims 2-9 recite the limitation "up to about 427 amino acids in length", since the term "about" has not been defined in the specification as it relates to size, i.e. how many amino acids above and below 427 are encompassed, 456 amino acids are considered to be within the range recited. Therefore, the polypeptide of Han et al. anticipate the claims as written. Furthermore, Han et al. teaches how to perform phosphodiesterase assays on the splice variant as well as the measurement of PDE activity in the presence of the inhibitor rolipram (page 16153, right column, PDE assays). Since claim 53 is directed to a kit to screen for compounds that inhibit PDE7 activity wherein said kit comprises the polypeptide having PDE activity and the reagents required to measure PDE activity, the teachings of Han et al. also anticipate the instant claim as written.

24. Claims 1-11, 19 and 53 are rejected under 35 U.S.C. 102(b) as being anticipated by Hoffmann et al. (Cell Biochem. Biophys 28:103-113, 1998; Swiss Prot Accession Number O08593). Hoffman et al. teaches a rat PDE7 which is 426 amino acids long. It is 94.1% sequence identical to the polypeptide of SEQ ID NO: 1. See attached alignment. Claims 1-11 and 19 are directed in part to a human, mouse or rat phosphodiesterase comprising a phosphodiesterase 7 catalytic domain wherein said phosphodiesterase is a

structural homolog of a polypeptide comprising at least 312 amino acids of SEQ ID NO: 1. Therefore, the polypeptide of Hoffmann et al. anticipates the instant claims as written.

Claim Rejections - 35 USC § 103

25. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

26. This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

27. Claim 53 is rejected under 35 U.S.C. 103(a) as being unpatentable over Hoffmann et al. (Cell Biochem. Biophys 28:103-113, 1998; Swiss Prot Accession Number O08593) in view of Han et al. (J. Biol. Chem. 272(26):16152-16157, 1997). The teachings of Hoffmann et al. and Han et al. have been disclosed above. Hoffmann et al. teaches that further experiments with the PDE7 exposed to different inhibitors is needed to further characterize the PDE7 (page 111, last paragraph), however the reference does not teach a kit to screen for compounds that inhibit PDE7 activity.

Claim 53 is directed to a kit to screen for compounds that inhibit PDE7 activity wherein said kit comprises a polypeptide having PDE activity and the reagents required to measure PDE activity.

It would have been obvious to one of ordinary skill in the art at the time the invention was made to make a kit to screen for compounds that inhibit PDE7 activity wherein said kit comprises the polypeptide of Hoffmann et al. as well as reagents to measure PDE7 activity. A person of ordinary skill in the art is motivated to make such kit because Hoffmann et al. suggests testing different inhibitors for further characterization of the PDE7 and also because it is well known in the art that screening for inhibitors of PDE7 activity is one of the techniques known which allow further characterization of PDE enzymes. PDEs are classified based on their structure, substrate specificity, inhibitor sensitivity and allosteric cofactors. One of ordinary skill in the art has a reasonable expectation of success at making the kit since Han et al. teaches measuring PDE activity in the presence of the inhibitor rolipram to further characterize the splice variant. Therefore, the invention as a whole would have been prima facie obvious to a person of ordinary skill in the art at the time the invention was made.

Conclusion

28. No claim is in condition for allowance.

29. Certain papers related to this application may be submitted to Art Unit 1652 by facsimile transmission. The FAX number is (703) 872-9306. The faxing of such papers must conform with the notices published in the Official Gazette, 1156 OG 61 (November 16, 1993) and 1157 OG 94 (December 28, 1993) (see 37 CFR 1.6(d)). NOTE: If Applicant submits a paper by FAX, the original copy should be retained by Applicant or Applicant's representative. NO DUPLICATE COPIES SHOULD BE SUBMITTED, so as to avoid the processing of duplicate papers in the Office.

30. Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PMR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should

you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

31. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Delia M. Ramirez whose telephone number is (571) 272-0938. The examiner can normally be reached on Monday-Friday from 8:30 AM to 5:00 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Dr. Ponnathapura Achutamurthy can be reached on (571) 272-0928. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 308-1234.

Delia M. Ramirez, Ph.D.
Patent Examiner
Art Unit 1652

DR
June 8, 2004

REBECCA E. PRUTY
PRIMARY EXAMINER
GROUP ~~1800~~ 1600

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2004, 09:24:28 ; Search time 18 Seconds
(without alignments)
1232.327 Million cell updates/sec

Title: US-09-966-781A-1
Perfect score: 2243
Sequence: 1 DQTALYIRMLGDVRVRSRAG.....DTDAAFELNSQLLPQENRLS 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2243	100.0	482	1	CN7A_HUMAN	Q13946 homo sapien
2	2116	94.3	426	1	CN7A_RAT	O08593 rattus norv
3	2105	93.8	456	1	CN7A_MOUSE	P70453 mus musculu
4	1403.5	62.6	450	1	CN7B_HUMAN	Q9np56 homo sapien
5	1391.5	62.0	446	1	CN7B_MOUSE	Q9qxq1 mus musculu
6	555	24.7	844	1	CN4A_RAT	P54748 rattus norv
7	551	24.6	844	1	CN4A_MOUSE	O89084 mus musculu
8	550	24.5	721	1	CN4B_RAT	P14646 rattus norv
9	550	24.5	736	1	CN4B_HUMAN	Q07343 homo sapien
10	545	24.3	712	1	CN4C_HUMAN	Q08493 homo sapien
11	542	24.2	809	1	CN4D_HUMAN	Q08499 homo sapien
12	541	24.1	886	1	CN4A_HUMAN	P27815 homo sapien
13	539	24.0	672	1	CN4D_RAT	P14270 rattus norv
14	534.5	23.8	536	1	CN4C_RAT	P14644 rattus norv
15	503	22.4	829	1	CN8A_HUMAN	O60658 homo sapien
16	498.5	22.2	823	1	CN8A_MOUSE	O88502 mus musculu
17	493.5	22.0	549	1	YST1_CAEEL	Q22000 caenorhabdi
18	482	21.5	664	1	YFGK_CAEEL	O18696 caenorhabdi
19	478.5	21.3	777	1	CNA1_DROME	P12252 drosophila
20	471.5	21.0	793	1	REGA_DICDI	Q23917 dictyosteli
21	471.5	21.0	885	1	CN8B_HUMAN	O95263 homo sapien
22	470.5	21.0	534	1	CN1B_BOVIN	Q01061 bos taurus
23	470.5	21.0	535	1	CN1B_MOUSE	Q01065 mus musculu
24	469.5	20.9	535	1	CN1B_RAT	Q01066 rattus norv
25	466	20.8	654	1	CN1C_MOUSE	Q64338 mus musculu
26	461	20.6	768	1	CN1C_RAT	Q63421 rattus norv
27	457.5	20.4	536	1	CN1B_HUMAN	Q01064 homo sapien
28	456.5	20.4	565	1	CN1A_MOUSE	Q61481 mus musculu
29	452	20.2	534	1	CN1A_HUMAN	P54750 homo sapien
30	452	20.2	709	1	CN1C_HUMAN	Q14123 homo sapien
31	439.5	19.6	529	1	CN1A_BOVIN	P14100 bos taurus
32	418	18.6	534	1	CN9A_MOUSE	O70628 mus musculu
33	412	18.4	593	1	CN9A_HUMAN	O76083 homo sapien
34	402.5	17.9	1112	1	CN3B_HUMAN	Q13370 homo sapien
35	385.5	17.2	1108	1	CN3B_RAT	Q63085 rattus norv
36	385	17.2	799	1	CN3B_MOUSE	Q61409 mus musculu
37	375	16.7	1141	1	CN3A_HUMAN	Q14432 homo sapien
38	363	16.2	1141	1	CN3A_RAT	Q62865 rattus norv
39	348.5	15.5	865	1	CN5A_CANFA	O77746 canis famil
40	347.5	15.5	875	1	CN5A_HUMAN	O76074 homo sapien
41	336.5	15.0	833	1	CN5A_RAT	O54735 rattus norv
42	336.5	15.0	865	1	CN5A_MOUSE	Q8cg03 mus musculu
43	332.5	14.8	865	1	CN5A_BOVIN	Q28156 bos taurus
44	327	14.6	921	1	CN2A_BOVIN	P14099 bos taurus
45	323	14.4	928	1	CN2A_RAT	Q01062 rattus norv

ALIGNMENTS

```
RESULT 1
CN7A_HUMAN
ID   CN7A_HUMAN     STANDARD;      PRT;   482 AA.
AC   Q13946; O15380;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A
DE   (EC 3.1.4.17) (HCP1) (TM22).
GN   PDE7A.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM PDE7A1).
RX   MEDLINE=93286141; PubMed=8389765;
RA   Michaeli T., Bloom T.J., Martins T., Loughney K., Ferguson K.,
RA   Riggs M., Rodgers L., Beavo J.A., Wigler M.;
RT   "Isolation and characterization of a previously undetected human cAMP
RT   phosphodiesterase by complementation of cAMP phosphodiesterase-
RT   deficient Saccharomyces cerevisiae.";
RL   J. Biol. Chem. 268:12925-12932(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM PDE7A2).
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=97341143; PubMed=9195912;
RA   Han P., Zhu X., Michaeli T.;
RT   "Alternative splicing of the high affinity cAMP-specific
RT   phosphodiesterase (PDE7A) mRNA in human skeletal muscle and heart.";
RL   J. Biol. Chem. 272:16152-16157(1997).
CC   -!- FUNCTION: Plays a role in signal transduction by regulating the
CC       intracellular concentration of cyclic nucleotides. This
CC       phosphodiesterase is highly specific for cAMP and may have a role
CC       in muscle signal transduction.
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- COFACTOR: Requires divalent cations.
CC   -!- ENZYME REGULATION: Insensitive to all selective PDE inhibitors.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- SUBCELLULAR LOCATION: PDE7A1 (57 KDA) IS LOCATED MOSTLY TO SOLUBLE
CC       CELLULAR FRACTIONS. PDE7A2 (50 KDA) IS LOCATED TO PARTICULATE
CC       CELLULAR FRACTIONS.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=PDE7A1;
CC         IsoId=Q13946-1; Sequence=Displayed;
CC       Name=PDE7A2;
CC         IsoId=Q13946-2; Sequence=VSP_004593;
CC   -!- TISSUE SPECIFICITY: PDE7A1 is found at high levels in skeletal
CC       muscle and at low levels in a variety of tissues including brain
CC       and heart. It is expressed as well in two T-cell lines. PDE7A2 is
CC       found abundantly in skeletal muscle and at low levels in heart.
CC   -!- DEVELOPMENTAL STAGE: Developmentally regulated. PDE7A1 and PDE7A2
CC       are found in several fetal tissues, expression is reduced
CC       throughout development. It persists strongly only in adult
```

```
CC       skeletal muscle.
CC   -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC       putative divalent metal sites and an N-terminal regulatory domain.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L12052; AAA35644.2; -.
DR   EMBL; U67932; AAB65772.1; -.
DR   Genew; HGNC:8791; PDE7A.
DR   MIM; 171885; -.
DR   GO; GO:0000267; C:cell fraction; NAS.
DR   GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS.
DR   GO; GO:0007165; P:signal transduction; NAS.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase; cAMP; Phosphorylation; Alternative splicing.
FT   DOMAIN       28     33       POLY-SER.
FT   DOMAIN      187    451       CATALYTIC (BY SIMILARITY).
FT   MOD_RES      84     84       PHOSPHORYLATION (POTENTIAL).
FT   VARSPLIC      1     46       MEVCYQLPVLPLDRPVPQHVLSRRGAISFSSSSALFGCPNP
FT                                RQLSQ -> MGITLIWCLALVLIKWITSK (in isoform
FT                                PDE7A2).
FT                                /FTId=VSP_004593.
SQ   SEQUENCE   482 AA;  55505 MW;  3B3C8F6E9154F88C CRC64;

  Query Match             100.0%;  Score 2243;  DB 1;  Length 482;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-176;
  Matches  426;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         57 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 116

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 176

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 236

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 296

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 356

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 416

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 476

Qy        421 QENRLS 426
              ||||||
Db        477 QENRLS 482
```

```
RESULT 2
CN7A_RAT
ID   CN7A_RAT       STANDARD;      PRT;   426 AA.
AC   O08593;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A
DE   (EC 3.1.4.17) (Rolipram-insensitive phosphodiesterase type 7)
DE   (Fragment).
GN   PDE7A.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98176136; PubMed=9515162;
RA   Hoffmann R., Abdel'Al S., Engels P.;
RT   "Differential distribution of rat PDE-7 mRNA in embryonic and adult
RT   rat brain.";
RL   Cell Biochem. Biophys. 28:103-113(1998).
CC   -!- FUNCTION: Plays a role in signal transduction by regulating the
CC       intracellular concentration of cyclic nucleotides. This
CC       phosphodiesterase is highly specific for cAMP and may have a role
CC       in muscle signal transduction (By similarity).
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- COFACTOR: Requires divalent cations (By similarity).
CC   -!- ENZYME REGULATION: Insensitive to all selective PDE inhibitors (By
CC       similarity).
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC       putative divalent metal sites and an N-terminal regulatory domain.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U77880; AAB51234.1; -.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase; cAMP.
FT   NON_TER       1      1
FT   DOMAIN      131    395       CATALYTIC (BY SIMILARITY).
SQ   SEQUENCE   426 AA;  49274 MW;  129BDC01C9351D26 CRC64;

  Query Match             94.3%;  Score 2116;  DB 1;  Length 426;
  Best Local Similarity   94.1%;  Pred. No. 3.2e-166;
  Matches  401;  Conservative    9;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              |||||||||||||||||||:|||||||||||||||:||||| ||||||||||||||
Db          1 DQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHAQSEIEASVSARNIRRLLSFQR 60

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              |||||||||| | |||||:||||||||||||||||||||||||||||||||||||||||
Db         61 YLRSSRFFRGATVCRSLNILDEDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        121 LFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              |||||||||||| :|| |||||||||||||||||||||||||:||| |:| |||||||||
Db        241 GLFSHLPLESRHEMEAQIGALILATDISRQNEYLSLFRSHLDKGDLHLDDGRHRHLVLQM 300

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              |||||||||||| |||||||||||||||||||||||||||||||||| ||||||||||
Db        301 ALKCADICNPCRNWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRQTESIANIQIGF 360

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              |||| ||||||||||:|||||||||||||||||||:| |||| ||||||||||
Db        361 MTYLQEPLFTEWARFSDTRLSQTMLGHVGLNKASWKGLQRQQPSSEDASAAFELNSQLLT 420

Qy        421 QENRLS 426
              ||||||
Db        421 QENRLS 426


RESULT 3
CN7A_MOUSE
ID   CN7A_MOUSE     STANDARD;      PRT;   456 AA.
AC   P70453; Q9ERB3;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A
DE   (EC 3.1.4.17) (P2A).
GN   PDE7A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=97098542; PubMed=8943082;
RA   Bloom T.J., Beavo J.A.;
RT   "Identification and tissue-specific expression of PDE7
RT   phosphodiesterase splice variants.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:14188-14192(1996).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Brain, and Testis;
RX   MEDLINE=20483661; PubMed=11027622;
RA   Wang P., Wu P., Egan R.W., Billah M.M.;
RT   "Cloning, characterization, and tissue distribution of mouse
RT   phosphodiesterase 7A1.";
RL   Biochem. Biophys. Res. Commun. 276:1271-1277(2000).
CC   -!- FUNCTION: Plays a role in signal transduction by regulating the
CC       intracellular concentration of cyclic nucleotides. This
CC       phosphodiesterase is highly specific for cAMP and may have a role
CC       in muscle signal transduction.
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- COFACTOR: Requires divalent cations.
CC   -!- ENZYME REGULATION: Insensitive to all selective PDE inhibitors.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1; Synonyms=PDE7A2;
CC         IsoId=P70453-1; Sequence=Displayed;
CC       Name=2; Synonyms=PDE7A1;
CC         IsoId=P70453-2; Sequence=VSP_004594;
CC   -!- TISSUE SPECIFICITY: Widely expressed with highest levels in the
CC       skeletal muscle.
CC   -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC       putative divalent metal sites and an N-terminal regulatory domain.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U68171; AAB08479.1; -.
DR   EMBL; AY007702; AAG16295.1; -.
DR   MGD; MGI:1202402; Pde7a.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase; cAMP; Alternative splicing.
FT   DOMAIN      161    425       CATALYTIC (BY SIMILARITY).
FT   VARSPLIC      1     20       MGITLIWCLALVLIKWITSK -> MEVCYQLPVLPLDRPVP
FT                                QHVLSRRGAISFSSSSALFGCPHPRQLSQ (in isoform
FT                                2).
FT                                /FTId=VSP_004594.
FT   CONFLICT    407    407       A -> D (IN REF. 2).
SQ   SEQUENCE   456 AA;  52441 MW;  0B826B96490D9F6E CRC64;

  Query Match             93.8%;  Score 2105;  DB 1;  Length 456;
  Best Local Similarity   93.7%;  Pred. No. 2.8e-165;
  Matches  399;  Conservative   13;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              |||||||||||||||||||||:||||||||||||||||:|| ||||||||||||||||
Db         31 DQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHSQSDIEASVSARNIRRLLSFQR 90

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              |||||| ||| | :||:|||:|||||||||||||||||||||||||||||||||||||||
Db         91 YLRSSRVFRGATVCSSLDILDEDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 150

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              |||||||||||||||:|||||||||||||||||||||||||||||||||||||||||:|
Db        151 LFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASS 210

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              |||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db        211 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNSSVLENHHWRSAVGLLRES 270

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              |||||||||||:|| |||||||||||||||||||||||||:||| |:| |||||||||
Db        271 GLFSHLPLESRQEMEAQIGALILATDISRQNEYLSLFRSHLDKGDLHLDDGRHRHLVLQM 330

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              |||||||||||| |||||||||||||||||||||||||||||||||| ||||||||||
Db        331 ALKCADICNPCRNWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRQTESIANIQIGF 390

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              |||||||||||||| ||||||||||||||||||||||:| |||| :||||||||||
Db        391 MTYLVEPLFTEWARFSATRLSQTMLGHVGLNKASWKGLQRQQPSSEDANAAFELNSQLLT 450

Qy        421 QENRLS 426
              ||||||
Db        451 QENRLS 456


RESULT 4
CN7B_HUMAN
ID   CN7B_HUMAN     STANDARD;      PRT;   450 AA.
AC   Q9NP56;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
```